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1645

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,307A

DATE: 08/08/2001

TIME: 14:38:55

Input Set : A:\ES.txt

Output Set: N:\CRF3\08082001\I828307A.raw

3 <110> APPLICANT: Mack, David
 4 Gish, Kurt
 5 Wilson, Keith
 7 <120> TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND
 METHODS OF

8 SCREENING FOR CANCER MODULATORS

10 <130> FILE REFERENCE: A-69192-1/DJB/JJD/AMS

C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/828,307A

C--> 12 <141> CURRENT FILING DATE: 2001-04-06

12 <150> PRIOR APPLICATION NUMBER: US 09/608,821

13 <151> PRIOR FILING DATE: 2000-06-30

15 <160> NUMBER OF SEQ ID NOS: 5

17 <170> SOFTWARE: PatentIn version 3.0

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 3794

21 <212> TYPE: DNA

22 <213> ORGANISM: Homo sapiens

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (38)..(2635)

28 <400> SEQUENCE: 1

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 30 Met Ala Leu Val Leu Gly

31 1 5

33 tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag 103

34 Ser Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln

35 10 15 20

37 cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca 151

38 Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala

39 25 30 35

41 aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att 199

42 Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile

43 40 45 50

45 ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat 247

46 Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp

47 55 60 65 70

49 ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc 295

50 Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser

51 75 80 85

53 aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att 343

54 Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile

55 90 95 100

57 gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg

58 Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu

59 105 110 115

61 ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt 439

62 Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg

63 120 125 130

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TECH CENTER 1600/2900

65	tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat	487
66	Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn	
67	135 140 145 150	
69	ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt	535
70	Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys	
71	155 160 165	
73	ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag	583
74	Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln	
75	170 175 180	
77	gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc	631
78	Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe	
79	185 190 195	
81	aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat	679
82	Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr	
83	200 205 210	
85	ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg	727
86	Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu	
87	215 220 225 230	
89	aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga	775
90	Asn Ser Ile Asn Ser Val Leu Gly Gly Ile Leu Asp Arg Leu Arg	
91	235 240 245	
93	ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg	823
94	Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala	
95	250 255 260	
97	atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag	871
98	Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys	
99	265 270 275	
101	agc ttg cac caa caa agt aca caa ctt agc agc agt ctg acc agc gtg	919
102	Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val	
103	280 285 290	
105	aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat	967
106	Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His	
107	295 300 305 310	
109	cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg	1015
110	Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu	
111	315 320 325	
113	aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt	1063
114	Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu	
115	330 335 340	
117	gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa	1111
118	Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln	
119	345 350 355	
121	cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa	1159
122	Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln	
123	360 365 370	
125	acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt	1207
126	Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly	
127	375 380 385 390	
129	tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc	1255

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130	Ser	Asp	Ile	Asp	Asn	Val	Thr	Gln	Arg	Leu	Pro	Ile	Gln	Asp	Ile	Leu
131						395				400						405
133	tca	gca	tcc	tct	tgt	tat	gtt	aat	aac	act	gaa	agt	tac	atc	cac	aga
134	Ser	Ala	Phe	Ser	Val	Tyr	Val	Asn	Asn	Thr	Glu	Ser	Tyr	Ile	His	Arg
135						410				415						420
137	aat	tta	cct	aca	ttg	gaa	gag	tat	gtt	tca	tac	tgg	tgg	ctg	ggf	ggc
138	Asn	Leu	Pro	Thr	Leu	Glu	Glu	Tyr	Asp	Ser	Tyr	Trp	Trp	Leu	Gly	Gly
139						425				430						435
141	ctg	gtc	atc	tgc	tct	ctg	ctg	acc	ctc	atc	gtg	att	ttt	tac	tac	ctg
142	Leu	Val	Ile	Cys	Ser	Leu	Leu	Thr	Leu	Ile	Val	Ile	Phe	Tyr	Tyr	Leu
143						440				445						450
145	ggc	tta	ctg	tgt	ggc	gtg	tgc	ggc	tat	gac	agg	cat	gcc	acc	ccg	acc
146	Gly	Leu	Leu	Cys	Gly	Val	Cys	Gly	Tyr	Asp	Arg	His	Ala	Thr	Pro	Thr
147	455					460				465						470
149	acc	cga	ggc	tgt	gtc	tcc	aac	acc	gga	ggc	gtc	ttc	ctc	atg	gtt	gga
150	Thr	Arg	Gly	Cys	Val	Ser	Asn	Thr	Gly	Gly	Val	Phe	Leu	Met	Val	Gly
151						475				480						485
153	gtt	gga	tta	agt	ttc	ctc	ttt	tgc	tgg	ata	ttg	atg	atc	att	gtg	gtt
154	Val	Gly	Leu	Ser	Phe	Leu	Phe	Cys	Trp	Ile	Leu	Met	Ile	Ile	Val	Val
155						490				495						500
157	ctt	acc	ttt	gtc	ttt	ggt	gca	aat	gtg	gaa	aaa	ctg	atc	tgt	gaa	cct
158	Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu	Lys	Leu	Ile	Cys	Glu	Pro
159						505				510						515
161	tac	acg	agc	aag	gaa	tta	ttc	cgg	gtt	ttg	gat	aca	ccc	tac	tta	cta
162	Tyr	Thr	Ser	Lys	Glu	Leu	Phe	Arg	Val	Leu	Asp	Thr	Pro	Tyr	Leu	Leu
163						520				525						530
165	aat	gaa	gac	tgg	gaa	tac	tat	ctc	tct	ggg	aag	cta	ttt	aat	aaa	tca
166	Asn	Glu	Asp	Trp	Glu	Tyr	Tyr	Leu	Ser	Gly	Lys	Leu	Phe	Asn	Lys	Ser
167	535					540				545						550
169	aaa	atg	aag	ctc	act	ttt	gaa	caa	gtt	tac	agt	gac	tgc	aaa	aaa	aat
170	Lys	Met	Lys	Leu	Thr	Phe	Glu	Gln	Val	Tyr	Ser	Asp	Cys	Lys	Lys	Asn
171						555				560						565
173	aga	ggc	act	tac	ggc	act	ctt	cac	ctg	cag	aac	agc	ttc	aat	atc	agt
174	Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln	Asn	Ser	Phe	Asn	Ile	Ser
175						570				575						580
177	gaa	cat	ctc	aac	att	aat	gag	cat	act	gga	agc	ata	agc	agt	gaa	ttg
178	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly	Ser	Ile	Ser	Ser	Glu	Leu
179						585				590						595
181	gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	ctg	ttg	ggt	gca	gca	gga
182	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe	Leu	Leu	Gly	Ala	Ala	Gly
183						600				605						610
185	aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	gga	ata	gac	aga	atg	aat
186	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys	Gly	Ile	Asp	Arg	Met	Asn
187	615					620				625						630
189	tat	gac	agc	tac	ttg	gct	cag	act	ggt	aaa	tcc	ccc	gca	gga	gtg	aat
190	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys	Ser	Pro	Ala	Gly	Val	Asn
191						635				640						645
193	ctt	tta	tca	ttt	gca	tat	gat	cta	gaa	gca	aaa	gca	aac	agt	ttg	ccc
194	Leu	Leu	Ser	Phe	Ala	Tyr	Asp	Leu	Glu	Ala	Lys	Ala	Asn	Ser	Leu	Pro

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195	650	655	660	
197	cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa			2071
198	Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys			
199	665	670	675	
201	aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act			2119
202	Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr			
203	680	685	690	
205	cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg			2167
206	Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu			
207	695	700	705	710
209	gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc			2215
210	Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe			
211	715	720	725	
213	atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat			2263
214	Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr			
215	730	735	740	
217	ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag			2311
218	Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu			
219	745	750	755	
221	ttc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct			2359
222	Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala			
223	760	765	770	
225	cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc			2407
226	Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro			
227	775	780	785	790
229	ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt			2455
230	Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu			
231	795	800	805	
233	ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg			2503
234	Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met			
235	810	815	820	
237	gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat			2551
238	Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn			
239	825	830	835	
241	atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att			2599
242	Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile			
243	840	845	850	
245	cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt			2645
246	His Asn Pro Val Met Thr Ser Pro Ser Gln His			
247	855	860	865	
249	tgaaaactgct tgagcatcag gatactcaa gtggaaagga tcacagattt ttggtagttt			2705
251	ctgggtctac aaggacttcc caaatccagg agcaacgcca gtggcaacgt agtgactcag			2765
253	gcgggcacca aggcaacggc accatggtc tctggtagt gctttaagaa tgaacacacaat			2825
255	cacgttatacg tccatggtcc atcactattc aaggatgact ccctcccttc ctgtctattt			2885
257	ttgtttttta ctttttaca ctgagttct atttagacac tacaacataat ggggtgtttt			2945
259	ttcccattgg atgcatttct atcaaaactc tatcaaatgt gatggctaga ttctaacata			3005
261	ttgccatgtg tggagtgtgc tgaacacaca ccagttaca ggaaagatgc attttgtgt			3065
263	cagtaaacgg tgtatataacc ttttgttacc acagagttt ttaaacaat gagtattata			3125
265	ggactttctt ctaaatgagc taaataagtc accattgact tcttggtgct gttaaaaata			3185

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267	atccattttc	actaaaagtg	tgtgaaacct	acagcatatt	cttcacgcag	agattttcat	3245
269	ctattatact	ttatcaaaga	ttggccatgt	tccacttgg	aatggcatgc	aaaagccatc	3305
271	atagagaaac	ctgcgttaact	ccatctgaca	aattcaaaag	agagagagag	atcttgagag	3365
273	agaaatgctg	ttcggtcaaa	agtggagttg	ttttaacaga	tgccaaattac	ggtgtacagt	3425
275	ttaacagagt	tttctgttgc	attaggataa	acattaattt	gagtgcagct	aacatgagta	3485
277	tcatcagact	agtatcaagt	gttctaaaat	gaaatatgag	aagatcctgt	cacaattctt	3545
279	agatctggtg	tccagcatgg	atgaaacctt	tgagtttgg	ccctaaattt	gcatgaaagc	3605
281	acaaggtaaa	tattcatttgc	ttcaggagt	ttcatgttgg	atctgtcatt	atcaaaaagtg	3665
283	atcagcaatg	aagaactggt	cggacaaaat	ttaacgttga	tgtaatggaa	ttccagatgt	3725
285	aggcattccc	cccaggtctt	tcatgtgca	gattgcagtt	ctgattcatt	tgaataaaaa	3785
287	ggaacttgg						3794
290	<210>	SEQ ID NO:	2				
291	<211>	LENGTH:	865				
292	<212>	TYPE:	PRT				
293	<213>	ORGANISM:	Homo sapiens				
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301	Ser Phe Ser	Gly Gly Gln	Pro Ser Ser	Thr Asp Ala	Pro Lys Ala	Trp	
302		20	25	30			
305	Asn Tyr Glu	Leu Pro Ala Thr	Asn Tyr Glu	Thr Gln Asp	Ser His	Lys	
306		35	40	45			
309	Ala Gly Pro	Ile Gly Ile	Leu Phe Glu	Leu Val His	Ile Phe	Leu Tyr	
310		50	55	60			
313	Val Val Gln	Pro Arg Asp	Phe Pro Glu Asp	Thr Leu Arg	Lys Phe	Leu	
314		65	70	75	80		
317	Gln Lys Ala	Tyr Glu Ser	Lys Ile Asp	Tyr Asp Lys	Pro Glu	Thr Val	
318		85	90	95			
321	Ile Leu Gly	Leu Lys Ile	Val Tyr Tyr	Glu Ala Gly	Ile Ile	Leu Cys	
322		100	105	110			
325	Cys Val Leu	Gly Leu Leu	Phe Ile	Ile Leu Met	Pro Leu	Val Gly	Tyr
326		115	120	125			
329	Phe Phe Cys	Met Cys Arg	Cys Asn Lys	Cys Gly	Gly Glu	Met His	
330		130	135	140			
333	Gln Arg Gln	Lys Glu Asn	Gly Pro Phe	Leu Arg Lys	Cys Phe	Ala Ile	
334		145	150	155	160		
337	Ser Leu Leu	Val Ile Cys	Ile Ile Ile	Ser Ile Gly	Ile Phe	Tyr Gly	
338		165	170	175			
341	Phe Val Ala	Asn His Gln	Val Arg Thr	Arg Ile Lys	Arg Ser	Arg Lys	
342		180	185	190			
345	Leu Ala Asp	Ser Asn Phe	Lys Asp	Leu Arg Thr	Leu Leu	Asn Glu	Thr
346		195	200	205			
349	Pro Glu Gln	Ile Lys Tyr	Ile Leu Ala	Gln Tyr Asn	Thr Thr	Lys Asp	
350		210	215	220			
353	Lys Ala Phe	Thr Asp Leu	Asn Ser Ile	Asn Ser Val	Leu Gly	Gly Gly	
354		225	230	235	240		
357	Ile Leu Asp	Arg Leu Arg	Pro Asn Ile	Ile Pro Val	Leu Asp	Glu Ile	
358		245	250	255			
361	Lys Ser Met	Ala Thr	Ala Ile	Lys Glu Thr	Lys Glu	Ala Leu	Asn

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <233> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

No